

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A primer₁ which amplifies *groEL2* gene fragment of at least one *Streptomyces* species₁ consisting of the nucleotide sequence of SEQ ID NO: 1.
2. (Currently Amended) A primer₁ which amplifies *groEL2* gene fragment of at least one *Streptomyces* species₁ consisting of the nucleotide sequence of SEQ ID NO: 2.
3. (Currently Amended) ~~[[A]] An isolated *groEL2* gene fragment derived from *Streptomyces* species or fragment thereof comprising~~ consisting of a polynucleotide ~~chosen from~~ selected from the group consisting of the nucleotide sequences of SEQ ID NOs: 3 to 42.
4. (Previously Presented) An isolated *groEL2* gene fragment from *S. scabiei* comprising SEQ ID NO: 43.
5. (Previously Presented) A method for identifying *Streptomyces* species comprising:
 - a) amplifying *groEL2* gene fragment of target microorganism using the primer according to claims 1 or 2;

b) analyzing the nucleotide sequence of the *groEL2* gene fragment thus amplified; and

c) comparing the nucleotide sequence obtained in b) with that of *groEL2* gene fragment of a reference strain.

6. (Previously Presented) The method of claim 5, wherein the microorganism is chosen from *R. equi*, *S. acrimycini*, *S. aculeolatus*, *S. alanosinicus*, *S. albireticuli*, *S. albofaciens*, *S. albogriseolus*, *S. alboniger*, *S. albus*, *S. ambofaciens*, *S. aminophilus*, *S. anandii*, *S. argenteolus*, *S. bambergiensis*, *S. capillispiralis*, *S. carpinesis*, *S. catenulae*, *S. cellulosa*, *S. chartreusis*, *S. chattanoogensis*, *S. cinereoruber*, *S. cinnamomensis*, *S. cirratus*, *S. coeruleorubidus*, *S. collinus*, *S. corchorusii*, *S. diastaticus*, *S. djakartensis*, *S. erumpens*, *S. fulvissimus*, *S. galilaeus*, *S. griseochromogenes*, *S. griseolus*, *S. griseoviridis*, *S. humiferus*, *S. hygrosopicus*, *S. minutiscleroticus*, *S. murinus*, *S. nodosus*, *T. paurometabola*, *S. acidiscabies*, *S. bottropensis*, *S. disastatochromogenes*, *S. neyagawaensis*, *S. scabiei*, and *S. turgidiscabies*.

7. (Original) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

8. (Original) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.

9. (Original) The method of claim 5, wherein c) further comprises multi-aligning the nucleotide sequences and forming a phylogenetic tree.

10 - 11. (Cancelled)

12. (Previously Presented) The *groEL2* gene fragment of claim 4, wherein the fragment is SEQ ID NO: 43.

13. (Currently Amended) An isolated *groEL2* gene fragment ~~derived~~ from a potato scab pathogenic microorganism ~~comprising~~ consisting of a polynucleotide ~~chosen from~~ selected from the group consisting of the nucleotide sequences of any one of SEQ ID NOs: 44 to 61.

14. (Previously Presented) An isolated *groEL2* gene fragment produced by amplification from a microorganism using

a) a primer consisting of the nucleotide sequence of SEQ ID NO: 1 and

b) a primer consisting of the nucleotide sequence of SEQ ID NO: 2,

wherein said microorganism is selected from the group consisting of *R. equi*, *S. acrimycini*, *S. aculeolatus*, *S. alanosinicus*, *S. albireticuli*, *S. albofaciens*, *S. albogriseolus*, *S. alboniger*, *S. albus*, *S. ambofaciens*, *S. aminophilus*, *S. anandii*, *S. argenteolus*, *S. bambergiensis*, *S. capillispiralis*, *S. carpinesis*, *S. catenulae*, *S. cellulosa*, *S. chartreusis*, *S. chattanoogensis*, *S. cinereoruber*, *S. cinnamomensis*, *S. cirratus*, *S. coeruleorubidus*, *S. collinus*, *S. corchorusii*, *S. diastaticus*, *S. djakartensis*, *S. erumpens*, *S. fulvissimus*, *S. galilaeus*, *S. griseochromogenes*, *S. griseolus*, *S.*

griseoviridis, *S. humiferus*, *S. hygrosopicus*, *S. minutiscleroticus*, *S. murinus*, *S.*
nodosus, *T. paurometabola*, *S. acidiscabies*, *S. bottropensis*, *S. disastatochromogenes*,
S. neyagawaensis, *S. scabiei*, and *S. turgidiscabies*.